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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: Wed Jun 27 06:52:47 EDT 2007

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Application No: 10584082 Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-21 15:58:53.503
Finished: 2007-06-21 15:58:55.725
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 222 ms
Total Warnings: 40
Total Errors: 6
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

Input Set:

Output Set:

Started: 2007-06-21 15:58:53.503
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Total Warnings: 40
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No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (37)
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SEQUENCE LISTING

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GENES AND USE OF THE SAME

<130> 47236-0009-00-US

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<141> 2007-06-21

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<151> 2006-06-22

<150> PCT/JP04/19196

<151> 2004-12-22

<150> JP 2003-425673

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<170> PatentIn Ver. 3.3

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Gly Gly Leu Trp Ser Lys Trp Gly Thr Gly Ser Asn Leu Ser Phe Val

15 20 25

tcg cgc aag gag cag cag cag cag cag cag agc tct ccc gag gcg 387

Ser Arg Lys Glu Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala

30 35 40 45

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Ser Thr Pro Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile

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ccc gag ggc ttc ttg acc gtg gag gag gtg tcg aag cac gac aat ccg			483
Pro Glu Gly Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro			
65	70	75	
agc gac tgc tgg atc gtc atc aac gac aag gtg tac gac gtg agc gca			531
Ser Asp Cys Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala			
80	85	90	
ttc ggg aag acg cat ccg ggc ggc cct gtg atc ttc acg cag gcc ggc			579
Phe Gly Lys Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly			
95	100	105	
cgc gac gcc acg gat tct ttc aag gtt ttc cac tcc gcc aag gcg tgg			627
Arg Asp Ala Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp			
110	115	120	125
cag ttt ctc cag gac ctg tac atc gga gat ctg tac aat gcc gag cca			675
Gln Phe Leu Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro			
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Val Ser Glu Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met			
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Arg Ser Gln Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys			
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Ser Gln Thr Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu			
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ttc tgg cag caa tgt gga tgg tta tcg cac gat ttt ctc cac cac cag			915
Phe Trp Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln			
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Gly Asn Phe Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His			
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Asn Val His His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro			
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Ile Asp Pro Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu			
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Ile Leu Ala Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val			
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cag cac ctt ctg ttc ttc ccg ctc ctc ttc ttg gca aga ttc agc tgg			1203
Gln His Leu Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp			
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Leu His Ser Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr			
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Ile Gly Ala Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp			
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ctc ttc ttg tcg caa ctg ttt tgc ggc gct ctg ctc agc att gtc ttc			1395
Leu Phe Leu Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe			
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gtg atc agc cac aat ggc atg gat gtg tac aac gac ccc cgg gac ttc			1443
Val Ile Ser His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe			
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gtg acg gcc caa gtc acc tcg acc aga aac atc gaa ggc aac ttc ttc			1491
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Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val			
430	435	440	445
aag gcg ctc tgc gcc aag cac ggt ttg cat tac gaa gaa ttg agt ctg			1635
Lys Ala Leu Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu			
450	455	460	
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Gly Thr Gly Val Cys Arg Val Phe Asn Arg Leu Val Glu Val Ala Tyr			
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gct gcg aaa gta tag atcgacgaga gtttcccacc aacacagtta gaacaaggga			1738
Ala Ala Lys Val			
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cgaatatacg tctccacgccc ttcaagtttc agcttcaact gattgtcttc agtaaccatc			1858

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<213> Marchantia polymorpha

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35 40 45
Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile Pro Glu Gly
50 55 60
Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys
65 70 75 80
Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala Phe Gly Lys
85 90 95
Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala
100 105 110
Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu
115 120 125
Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu
130 135 140

Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met Arg Ser Gln
145 150 155 160

Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys Val Thr Asn
165 170 175

Phe Ala Ile Leu Ala Ala Ser Leu Ala Val Ile Ala Trp Ser Gln Thr
180 185 190

Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu Phe Trp Gln
195 200 205

Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val Thr Glu
210 215 220

Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp Gly Asn Phe
225 230 235 240

Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His Asn Val His
245 250 255

His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro Ile Asp Pro
260 265 270

Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu Ile Leu Ala
275 280 285

Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val Gln His Leu
290 295 300

Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp Leu His Ser
305 310 315 320

Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr Met Arg Trp
325 330 335

Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser Ile Gly Ala
340 345 350

Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp Leu Phe Leu
355 360 365

Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe Val Ile Ser
370 375 380

His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe Val Thr Ala
385 390 395 400

Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe Asn Asp Trp
405 410 415

Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Ser
420 425 430

Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val Lys Ala Leu
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cgaatccgcc gagagtcgat cgggattggg tagaaggagg agaaggagga gaagaggagg 180

aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229
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Lys Thr Val Phe Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu
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acg gaa tct gcg atc acc aaa ggt ttg cca tgc gtc gat agc ccg acg 325
Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr
30 35 40

ccg atc gtt ctt ggg ttg tcg tcc tac ttg aca ttc gtg ttt ctc ggg 373
Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly
45 50 55 60

ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421
Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro
65 70 75

gcc att ttg aac ctg ttt gtg atc ttc cac aac ttc gtc tgc ttc gca 469
Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala
80 85 90

ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517
Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn
95 100 105

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Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met

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175	180	185	
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225	230	235	
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